APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/529,232	04/10/2000	YASUO KONISHI	2139-11US-FC	1386

20988   7590   11/06/2002

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EXAMINER
SHEINBERG, MONIKA B

ART UNIT	PAPER NUMBER
1634	

DATE MAILED: 11/06/2002

_9_

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 07-01)

Sequence Compliance

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR § 1.821(a)(1) and (a)(2). It is acknowledged that there is an indication of the Sequence Listing in computer readable format. Unfortunately, this application fails to comply with the requirements of 37 CFR § 1.821 through 1.825 because of two issues: 1) SEQ ID NO: 3 is in improper format due to each version of SEQ ID NO: 3 being different and distinct amino acid sequences thus requiring individual sequence identifiers **per** sequence in the sequence listing and the specification; and 2) please see the reasons listed in the attached Raw Sequence Listing Error Report. Thus, it is requested that the applicant send in another copy of the computer readable format. Please provide another statement as per 37 CFR § 1.821 (f) stating that the Paper Listing and the computer readable format are the same. Applicant is reminded that CD-ROM sequence listings are now accepted instead of a paper copy of the sequence listing for the specification. Applicant(s) are given the same response time regarding this failure to comply as that set forth to respond to this office action. Applicant is required to complete the response within a time limit of one month from the date of this letter or as extended as follows. AN EXTENSION OF THIS TIME LIMIT MAY BE GRANTED UNDER EITHER 37 CFR § 1.136 (a) OR (b) UP TO A MAXIMUM OF SIX MONTHS.

Inquiries

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR § 1.6(d)). The CM1 Fax Center number is (703) 308-4242.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Monika B. Sheinberg, whose telephone number is (703) 306-0511. The examiner can normally be reached on Monday-Friday from 1 P.M to 8 P.M. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones, can be reached on (703) 308-1152.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to Patent Analyst, Chantae Dessau, whose telephone number is (703) 605-1237, or to the Technical Center receptionist whose telephone number is (703) 308-0196.
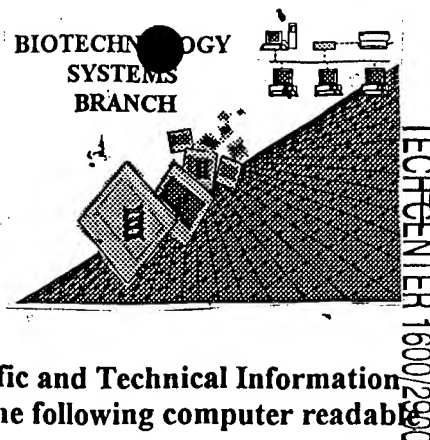
October 25, 2002
Monika B. Sheinberg
Art Unit 1634 *MBS*

ENCLOSED: Raw Sequence Listing Error Report

JEHANNE SOUAYA
PATENT EXAMINER
11/4/02

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/529,232_

Source: _1600_

Date Processed by STIC: _12/4/01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/529,232

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics
Wrapped Aminos ·
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   'SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213> Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

1600

```
RAW SEQUENCE LISTING                    DATE: 12/04/2001
PATENT APPLICATION:  US/09/529,232      TIME: 14:09:17

     Input Set : A:\SEQLIST1.txt
     Output Set: N:\CRF3\11212001\I529232.raw
```

Does Not Comply
Corrected Diskette Needed

```
      4 <110> APPLICANT: PRESCOTT, CATHERINE DENISE
      6 <120> TITLE OF INVENTION: METHODS FOR MODULATING GENE EXPRESSION
      9 <130> FILE REFERENCE: GM50040
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/529,232
     12 <141> CURRENT FILING DATE: 2000-04-06
     14 <150> PRIOR APPLICATION NUMBER: PCT/US98/21052
     15 <151> PRIOR FILING DATE: 1998-10-07
     17 <150> PRIOR APPLICATION NUMBER: 60/061,218
     18 <151> PRIOR FILING DATE: 1997-10-07
     20 <160> NUMBER OF SEQ ID NOS: 3
     22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
     24 <210> SEQ ID NO: 1
     25 <211> LENGTH: 38
     26 <212> TYPE: RNA
     27 <213> ORGANISM: Homo sapiens
     29 <220> FEATURE:
     30 <221> NAME/KEY: unsure
     31 <222> LOCATION: (15)(16)(17)(18)
     32 <223> OTHER INFORMATION: Wherein n can be represented by a, c, g, or u
     34 <400> SEQUENCE: 1
W--> 35 gggucagccc uaggnnnncc uagguaagca auggaccc                   38
     37 <210> SEQ ID NO: 2
     38 <211> LENGTH: 14
     39 <212> TYPE: RNA
     40 <213> ORGANISM: Homo sapiens
     42 <220> FEATURE:
     43 <221> NAME/KEY: unsure
     44 <222> LOCATION: (1)(2)(3)(4)(5)(9)(10)(11)(12)(13)(14)
     45 <223> OTHER INFORMATION: Wherein n can be represented by a, c, g, or u
     47 <400> SEQUENCE: 2
W--> 48 nnnnnagcnn nnnn                                             14
     50 <210> SEQ ID NO: 3
     51 <211> LENGTH: 19
     52 <212> TYPE: RNA
     53 <213> ORGANISM: Homo sapiens
     55 <220> FEATURE:
     56 <221> NAME/KEY: unsure
     57 <222> LOCATION: (1)(2)(3)(4)(5)(6)(7)(15)(16)(17)(18)(19)
     59 <400> SEQUENCE: 3
W--> 60 nnnnnnuaag caaunnnnn                                        19
```

<223> was omitted
See error summary sheet,
item 9

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/529,232**

DATE: 12/04/2001
TIME: 14:09:18

Input Set : **A:\SEQLIST1.txt**
Output Set: **N:\CRF3\11212001\I529232.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:60 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3